



SEQUENCE LISTING

<110> University of Victoria Innovation and Development
Corporation
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Eades, Caleb Joshua

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Asp Leu Leu Lys Gly Pro Ala Ala Gly Leu Val Asp Asp Ser Arg Val
 130 135 140

Asp Val Leu Leu Glu Gln Ser Gln Asn Leu Ala Glu Val Leu Lys Phe
 145 150 155 160

Ala Phe Asp Thr Pro Ser Gly Val Pro Thr Asn Met Ile Asn Ile Thr
 165 170 175

Ser Gly Gly Asn Asp Gly Ala Thr Thr Asn Gly Leu Ala Val Thr Gly
 180 185 190

Thr Leu Val Leu Glu Trp Thr Arg Leu Ser Asp Leu Thr Gly Asn Asp
 195 200 205

Glu Thr Ala Arg Leu Ser Gln Arg Ala Glu Asp Thr Leu Leu His Pro
 210 215 220

Glu Pro Ala Gln Thr Glu Pro Phe Pro Gly Leu Ile Gly Ser Ala Val
 225 230 235 240

Asn Ile Ala Asp Gly Lys Leu Ala Asn Gly His Ile Ser Trp Asn Gly
 245 250 255

Gly Ala Asp Ser Thr Thr Glu Thr Leu Ile Lys Met Thr Val Thr Asp
 260 265 270

Pro Glu Arg Phe Gly Leu Thr Arg Asp Arg Trp Val Ala Ala Ala Glu
 275 280 285

Ser Ser Ile Asn His Leu Ala Ser His Pro Ser Thr Arg Pro Asp Val
 290 295 300

Thr Phe Leu Ala Thr Thr Asn Glu Glu His Gln Leu Gly Leu Thr Ser
 305 310 315 320

Gln His Leu Thr Cys Phe Asp Gly Gly Ser Phe Leu Leu Gly Gly Thr
 325 330 335

Leu Leu Asp Arg Gln Asp Phe Val Asp Phe Gly Leu Asp Leu Val Ala
 340 345 350

Gly Cys His Glu Thr Thr Asn Ser Thr Leu Thr Gly Ile Gly Pro Glu
 355 360 365

Gln Phe Ser Trp Asp Pro Asn Gly Val Pro Asp Ser Gln Lys Glu Leu
 370 375 380

Phe Glu Arg Ala Gly Phe Thr Ile Asn Ser Gly Gln Thr Ile Leu Arg
 385 390 395 400

Pro Glu Val Ile Glu Ser Phe Thr Thr Ala Trp Arg Val Thr Gly Asp
 405 410 415

Gly Thr Thr Leu Glu Trp Val Trp Asn Ala Phe Thr Asn Ile Asn Lys
 420 425 430

Thr Cys Arg Thr Ala Thr Gly Phe Ala Gly Leu Glu Asn Val Asn Ala
 435 440 445

Ala Asn Gly Gly Gly Arg Ile Asp Asn Gln Glu Ser Phe Met Phe Ala
 450 455 460

Glu Val Leu Lys Thr Ser Phe Leu Thr Phe Ala Pro Glu Asp Asp Trp
 465 470 475 480

Gln Val Gln Lys Gly Ser Gly Asn Thr Phe Val Thr Asn Thr Glu Ala
 485 490 495

His Pro Phe Lys Val Thr Thr Pro Gln
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<400> 7
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6

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Gly Gly Leu Gly Glu Ser Phe Thr Glu Thr
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<400> 14

Leu Ala Glu Thr Leu Lys Thr Leu Thr
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<222> (9)..(9)

<223> n is a, c, g, or t/u

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 <222> (15)..(15)
 <223> r is g or a

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 ggyggyctng gygartcntt ctacgagta

29

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 <223> n is a, c, g, or t/u

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 <222> (28)..(28)
 <223> r is g or a

 <220>

<221> misc_feature
 <222> (29)..(29)
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 gtanaggtac ttnagngtct cngcnagrha gaa

33

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 Met Pro Arg Arg Trp Ser
 1 5

53

tcc ctc atc agc atc aca gcc atc ttc ttg gtc ctc ttc ttc ctc ctt
 Ser Leu Ile Ser Ile Thr Ala Ile Phe Leu Val Leu Phe Phe Leu Leu
 10 15 20

101

cat agg aat aca gac aca cca cgc gcc gcc aat agg gct aca aac ggc
 His Arg Asn Thr Asp Thr Pro Arg Ala Ala Asn Arg Ala Thr Asn Gly
 25 30 35

149

cct gcc aac ggc ttt gct agg cag caa agc ata tgt cca tca aca ccc
 Pro Ala Asn Gly Phe Ala Arg Gln Gln Ser Ile Cys Pro Ser Thr Pro
 40 45 50

197

cct cag cct cca tat aac cga acc agc acg gga ggg ttc aac tgg ggt
 Pro Gln Pro Pro Tyr Asn Arg Thr Ser Thr Gly Gly Phe Asn Trp Gly
 55 60 65 70

245

gaa atc cca gtc aga tac cct gta tcc gac ttc atc ccg ctg tca acc
 Glu Ile Pro Val Arg Tyr Pro Val Ser Asp Phe Ile Pro Leu Ser Thr
 75 80 85

293

aac tct cct gca aca ctt ccg cgc atc caa cgc tct tcc ttc cca ctt
 Asn Ser Pro Ala Thr Leu Pro Arg Ile Gln Arg Ser Ser Phe Pro Leu
 90 95 100

341

caa tcc tca atc act aaa tcc cgc cag gca gca gtc aaa ggt gcc ttt
 Gln Ser Ser Ile Thr Lys Ser Arg Gln Ala Ala Val Lys Gly Ala Phe
 105 110 115

389

cag cgc gca tgg acc tcc tac aca acc cac gcc tgg aag gcg gac gag
 Gln Arg Ala Trp Thr Ser Tyr Thr Thr His Ala Trp Lys Ala Asp Glu
 120 125 130

437

gta cgg ccc atc acg gcc gga tct cga aac aac ttt ggc gga tgg gga
 Val Arg Pro Ile Thr Ala Gly Ser Arg Asn Asn Phe Gly Gly Trp Gly
 135 140 145 150

485

gcg acc cta gtc gac aat ctc gac aca ctg cta atc atg ggg ctg gac

533

Ala Thr Leu Val Asp Asn Leu Asp Thr Leu Leu Ile Met Gly Leu Asp	
155 160 165	
gag gag ttc gca gcg gca gtc gac gcg ctc gca gat ata gaa ttc agc	581
Glu Glu Phe Ala Ala Val Asp Ala Leu Ala Asp Ile Glu Phe Ser	
170 175 180	
ccg cac tcg tcc cca tcc tcc tcc cag agc aca atc aac ata ttc gaa	629
Pro His Ser Ser Pro Ser Ser Ser Gln Ser Thr Ile Asn Ile Phe Glu	
185 190 195	
acg aca atc cgg tat ctg ggc ggc ttg ctc gcg gcg tat gat ctc act	677
Thr Thr Ile Arg Tyr Leu Gly Gly Leu Leu Ala Ala Tyr Asp Leu Thr	
200 205 210	
ggc tgt cga gag act cgg ctg ctg gac aaa gca atc cag ctt ggg gag	725
Gly Cys Arg Glu Thr Arg Leu Leu Asp Lys Ala Ile Gln Leu Gly Glu	
215 220 225 230	
atg atc tac acc tcc ttc gac aca gag aac cgc atg ccc gta cca cgg	773
Met Ile Tyr Thr Ser Phe Asp Thr Glu Asn Arg Met Pro Val Pro Arg	
235 240 245	
tgg aat ctg cac aaa gca ggc aac gga gag cct cag cgc gcg gca gtg	821
Trp Asn Leu His Lys Ala Gly Asn Gly Glu Pro Gln Arg Ala Ala Val	
250 255 260	
cag ggc gtg ctc gct gaa ctc gcc agc agc agt ctc gag ttc acg cgg	869
Gln Gly Val Leu Ala Glu Leu Ala Ser Ser Ser Leu Glu Phe Thr Arg	
265 270 275	
ctg tcg cag ctg acg ggg gat atg cgg tat ttc gat gcg gca tcc cgc	917
Leu Ser Gln Leu Thr Gly Asp Met Arg Tyr Phe Asp Ala Ala Ser Arg	
280 285 290	
att acc gat ctg ctt gac tcc caa gcc ggc cat acc cgg atc ccg ggg	965
Ile Thr Asp Leu Leu Asp Ser Gln Ala Gly His Thr Arg Ile Pro Gly	
295 300 305 310	
ttg tgg cca gtc agc gtg aac ctg cag aaa ggc gat ctg acc cgt ggg	1013
Leu Trp Pro Val Ser Val Asn Leu Gln Lys Gly Asp Leu Thr Arg Gly	
315 320 325	
tcg aca ttc agt ttt ggc ggg atg gcc gat agc gcc tac gag tat ctc	1061
Ser Thr Phe Ser Phe Gly Gly Met Ala Asp Ser Ala Tyr Glu Tyr Leu	
330 335 340	
ggc aag acg tat cgg ctc ctc ggt ggt gtg ggg aaa ggg cca cag tac	1109
Gly Lys Thr Tyr Arg Leu Leu Gly Gly Val Gly Lys Gly Pro Gln Tyr	
345 350 355	
gag cgt ctg gcg cga aac gca cta gat gcc ggg att cga cat ctc ctc	1157
Glu Arg Leu Ala Arg Asn Ala Leu Asp Ala Gly Ile Arg His Leu Leu	
360 365 370	
ttc cga ccg atg acg cct gat cat gca gat atc ctc cta ccc ggg gtc	1205
Phe Arg Pro Met Thr Pro Asp His Ala Asp Ile Leu Leu Pro Gly Val	
375 380 385 390	
gcg cac gca acc agc tct tcc gtg gga ctc gag ccc cgg aca gag cat	1253

Ala His Ala Thr Ser Ser Ser Val Gly Leu Glu Pro Arg Thr Glu His	
395 400 405	
ctc gcc tgt ttt gtg ggt ggg atg tac gcg ctc gcc ggg aag ctt ttc	1301
Leu Ala Cys Phe Val Gly Gly Met Tyr Ala Leu Ala Gly Lys Leu Phe	
410 415 420	
tca aac cag acg tac ctc gac acc ggc cgg aag ctg aca gac ggt tgt	1349
Ser Asn Gln Thr Tyr Leu Asp Thr Gly Arg Lys Leu Thr Asp Gly Cys	
425 430 435	
atc tgg tac tac gat aat tca ccg cta ggt atc atg ccg gag atg ttc	1397
Ile Trp Tyr Tyr Asp Asn Ser Pro Leu Gly Ile Met Pro Glu Met Phe	
440 445 450	
acc gtg ccg gct tgt ccg tca gtg gct gaa tgt cct tgg gac gaa aca	1445
Thr Val Pro Ala Cys Pro Ser Val Ala Glu Cys Pro Trp Asp Glu Thr	
455 460 465 470	
agg ggt ggt atc tac acc tac gtg cgt gat ggg cac tac ttt ctg cgt	1493
Arg Gly Gly Ile Tyr Thr Tyr Val Arg Asp Gly His Tyr Phe Leu Arg	
475 480 485	
cct gag gca atg gag agt atc ttc tat atg tgg cgc att aca ggg gac	1541
Pro Glu Ala Met Glu Ser Ile Phe Tyr Met Trp Arg Ile Thr Gly Asp	
490 495 500	
gaa aag tac cgc gag gct gca tgg aga atg ttc acg gct atc gaa gcg	1589
Glu Lys Tyr Arg Glu Ala Ala Trp Arg Met Phe Thr Ala Ile Glu Ala	
505 510 515	
gtt aca aag acg gag ttt ggg aat gcg gcg gtg cgg gat gtt atg gtt	1637
Val Thr Lys Thr Glu Phe Gly Asn Ala Ala Val Arg Asp Val Met Val	
520 525 530	
gag gaa gga aat gta aag aga gaa gat agc atg gag agt ttc tgg atg	1685
Glu Glu Gly Asn Val Lys Arg Glu Asp Ser Met Glu Ser Phe Trp Met	
535 540 545 550	
gca gag acg ttg aag tat ctg tat ctg ata ttt ggg gag acc gat ttg	1733
Ala Glu Thr Leu Lys Tyr Leu Tyr Leu Ile Phe Gly Glu Thr Asp Leu	
555 560 565	
gtc agc ttg gac gac tgg gtg ttc aat acg gag gcg cac cct ttg agg	1781
Val Ser Leu Asp Asp Trp Val Phe Asn Thr Glu Ala His Pro Leu Arg	
570 575 580	
ggg gca ggg agt tgacattgta ttcacacatc ggtatagaca aattatagag	1833
Gly Ala Gly Ser	
585	
tagacgttca aaacggccaa aactgaatgg atagactcca tatgcattga atatacaatg	1893
tattcgctgc aaagcatgga taaaataaag atgtacaaag tgtctttgtt gtcgctttga	1953
aagtggata tcatcccatc ataaggtggc agtgtaacca accctctata tcacctacat	2013
agacagctga tagaccggc	2032

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<400> 18

Met Pro Arg Arg Trp Ser Ser Leu Ile Ser Ile Thr Ala Ile Phe Leu
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Val Leu Phe Phe Leu Leu His Arg Asn Thr Asp Thr Pro Arg Ala Ala
 20 25 30

Asn Arg Ala Thr Asn Gly Pro Ala Asn Gly Phe Ala Arg Gln Gln Ser
 35 40 45

Ile Cys Pro Ser Thr Pro Pro Gln Pro Pro Tyr Asn Arg Thr Ser Thr
 50 55 60

Gly Gly Phe Asn Trp Gly Glu Ile Pro Val Arg Tyr Pro Val Ser Asp
 65 70 75 80

Phe Ile Pro Leu Ser Thr Asn Ser Pro Ala Thr Leu Pro Arg Ile Gln
 85 90 95

Arg Ser Ser Phe Pro Leu Gln Ser Ser Ile Thr Lys Ser Arg Gln Ala
 100 105 110

Ala Val Lys Gly Ala Phe Gln Arg Ala Trp Thr Ser Tyr Thr Thr His
 115 120 125

Ala Trp Lys Ala Asp Glu Val Arg Pro Ile Thr Ala Gly Ser Arg Asn
 130 135 140

Asn Phe Gly Gly Trp Gly Ala Thr Leu Val Asp Asn Leu Asp Thr Leu
 145 150 155 160

Leu Ile Met Gly Leu Asp Glu Glu Phe Ala Ala Ala Val Asp Ala Leu
 165 170 175

Ala Asp Ile Glu Phe Ser Pro His Ser Ser Pro Ser Ser Ser Gln Ser
 180 185 190

Thr Ile Asn Ile Phe Glu Thr Thr Ile Arg Tyr Leu Gly Gly Leu Leu
 195 200 205

Ala Ala Tyr Asp Leu Thr Gly Cys Arg Glu Thr Arg Leu Leu Asp Lys

210	215	220
Ala Ile Gln Leu Gly Glu Met Ile Tyr Thr Ser Phe Asp Thr Glu Asn		
225	230	235 240
Arg Met Pro Val Pro Arg Trp Asn Leu His Lys Ala Gly Asn Gly Glu		
	245	250 255
Pro Gln Arg Ala Ala Val Gln Gly Val Leu Ala Glu Leu Ala Ser Ser		
	260	265 270
Ser Leu Glu Phe Thr Arg Leu Ser Gln Leu Thr Gly Asp Met Arg Tyr		
	275	280 285
Phe Asp Ala Ala Ser Arg Ile Thr Asp Leu Leu Asp Ser Gln Ala Gly		
	290	295 300
His Thr Arg Ile Pro Gly Leu Trp Pro Val Ser Val Asn Leu Gln Lys		
305	310	315 320
Gly Asp Leu Thr Arg Gly Ser Thr Phe Ser Phe Gly Gly Met Ala Asp		
	325	330 335
Ser Ala Tyr Glu Tyr Leu Gly Lys Thr Tyr Arg Leu Leu Gly Gly Val		
	340	345 350
Gly Lys Gly Pro Gln Tyr Glu Arg Leu Ala Arg Asn Ala Leu Asp Ala		
	355	360 365
Gly Ile Arg His Leu Leu Phe Arg Pro Met Thr Pro Asp His Ala Asp		
	370	375 380
Ile Leu Leu Pro Gly Val Ala His Ala Thr Ser Ser Ser Val Gly Leu		
385	390	395 400
Glu Pro Arg Thr Glu His Leu Ala Cys Phe Val Gly Gly Met Tyr Ala		
	405	410 415
Leu Ala Gly Lys Leu Phe Ser Asn Gln Thr Tyr Leu Asp Thr Gly Arg		
	420	425 430
Lys Leu Thr Asp Gly Cys Ile Trp Tyr Tyr Asp Asn Ser Pro Leu Gly		
	435	440 445
Ile Met Pro Glu Met Phe Thr Val Pro Ala Cys Pro Ser Val Ala Glu		

450		455		460
Cys Pro Trp Asp Glu Thr Arg Gly Gly Ile Tyr Thr Tyr Val Arg Asp				
465		470		475 480
Gly His Tyr Phe Leu Arg Pro Glu Ala Met Glu Ser Ile Phe Tyr Met				
	485		490	495
Trp Arg Ile Thr Gly Asp Glu Lys Tyr Arg Glu Ala Ala Trp Arg Met				
	500		505	510
Phe Thr Ala Ile Glu Ala Val Thr Lys Thr Glu Phe Gly Asn Ala Ala				
	515		520	525
Val Arg Asp Val Met Val Glu Glu Gly Asn Val Lys Arg Glu Asp Ser				
	530		535	540
Met Glu Ser Phe Trp Met Ala Glu Thr Leu Lys Tyr Leu Tyr Leu Ile				
545		550		555 560
Phe Gly Glu Thr Asp Leu Val Ser Leu Asp Asp Trp Val Phe Asn Thr				
	565		570	575
Glu Ala His Pro Leu Arg Gly Ala Gly Ser				
	580		585	

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<400> 19
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